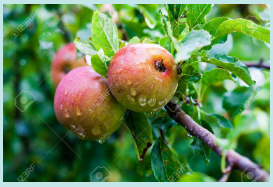
Genetic analysis of the morphological and ecophysiological responses to water deficit in an apple tree core-collection through a combination of high-throughput and physiological approaches



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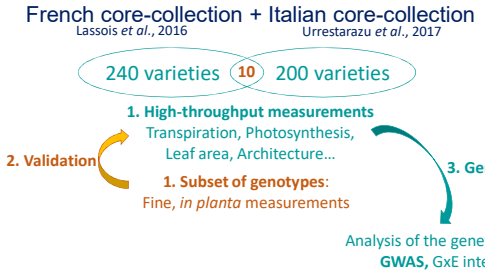
Context and objectives

In the face of increasing **water scarcity**, adapting **breeding** programs to target crops for more efficient water use is crucial. This requires a comprehensive knowledge of the plant physiological responses to drought, including the regulation of water status in plant tissues (by **stomatal closure**) and the determinants of **water-use efficiency** (the ratio of carbon gain to water use). These challenging questions have been scarcely studied in **perennial crops** such as apple tree, yet of major economic importance.
Here, we aim at screening the **European diversity of apple trees** responses to drought to decipher their genetic and physiological bases.

Montpellier (INRA Mauguio experimental unit)
240 x 4 trees = 960 trees

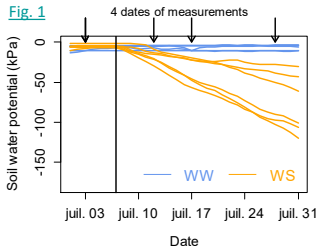


Bologna (UNIBO Bordone experimental unit)
200 x 2 trees = 400 trees

The deployment of **high-throughput phenotyping** methodologies in the **field** to screen large populations of trees is crucial to study the responses to drought and decipher the genetic architecture of their variability.

Methods and first results

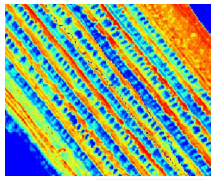
Fig. 1



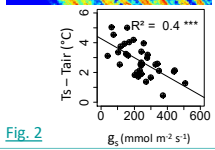
1. We imposed **two watering scenarios** to the core-collections by irrigation withholding.
The soil water status was monitored on 12 trees (6 for each scenario) equipped with tensiometers and capacitive sensors.
The water deficit was gradually established during the month of July, and Ψ_{soil} reach up to –120 kPa at the end of this period (Fig1).

2. In both sites, we characterized a subset of **10 varieties** for their responses all along the season.
Leaf water potential at predawn (Ψ_p), stem and leaf water potential at midday ($\Psi_{m,\,stem}$ and $\Psi_{m,\,leaf}$), stomatal conductance (g_s) and net photosynthesis (A_n) were measured at 4 dates (Fig 1). Marked contrasts were observed among the subset for their behaviours in WW and WS conditions.

3. We used high-throughput tools to measure the whole core-collection: airborne **imaging (thermal**, Fig 2; **and multispectral)**, **fluorimetry** (I_{PL}, Fig 3), terrestrial scanner **LIDAR** (Fig 4), and we assessed the robustness of correlations with the corresponding, fine *in planta* variables measured on the 10 varieties (respectively g_s, Fig 2; A_n, Fig 3; and an example for leaf area in Fig 4).



• **Thermal imaging** (Jones *et al.*, 1999)
Canopy temperature



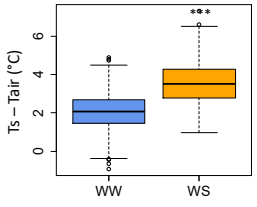
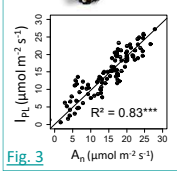


Fig. 2

• **I_{PL} method** (Losciale *et al.*, 2015)
I_{PL} ~ a*PSII + b*ΔT



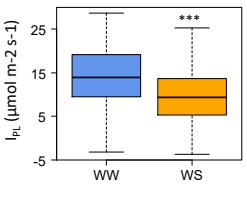
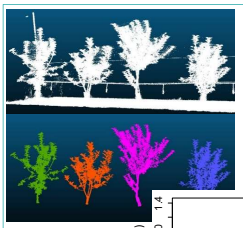
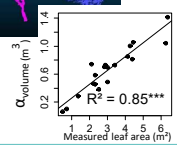


Fig. 3



• **LIDAR** (Boudon *et al.*, 2014)
Estimation of leaf area, plant height, canopy density, STAR…



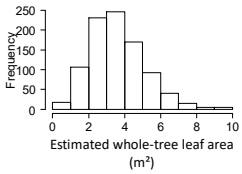


Fig. 4

A wide range of variability was found for all traits, with a highly significant effect of the genotype. **Mixed-models** including watering scenario and spatial effects were used to calculate BLUPs. **H^2** were medium to high ($0.40 < H^2 < 0.85$).

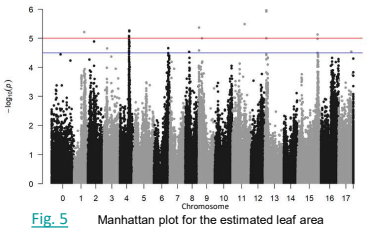


Fig. 5 Manhattan plot for the estimated leaf area

4. **GWAS** was undertaken on the high-throughput variables, with 275K SNPs issuing from a 400K array (LMM with per-chromosome Kinship (Rincent et al., 2014)). QTLs were detected for all traits (as exemplified for estimated leaf area in Fig 5). The analysis of QTLs colocations together with correlations between BLUPs is being performed to decipher the common bases to the responses to water deficit.

References

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